

BLAST

Basic Local Alignment Search Tool

[NCE/ BLAST/ Basic site/](#) **Formatting Results - NXA6CND801S**

gb|U94968.1| (1173 letters)

Query ID [gi120718751261182468.1.HVJ24918](#)
Description Hordeum vulgare hemoglobin gene, complete cds
Molecule type nucleic acid
Query Length 1173

Database Name nr
Description All GenBank+ EMBL+ DDBJ+ PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
Program BLASTN 2.2.25+

Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer PubChem BioAssay

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
U94968.1	Hordeum vulgare hemoglobin gene, complete cds	2167	2167	100%	0.0	100%	
U01229.1	Hordeum vulgare Harrington haemoglobin apoprotein (hb) mRNA, complete cds	883	1588	73%	0.0	100%	
HQ339021.1	Triticum aestivum clone UCDA00472 genomic sequence	405	405	29%	3e-109	87%	
DQ245217.1	Zea mays clone 13853 mRNA sequence	478	913	54%	8e-71	98%	
AF335504.1	Oryza sativa (japonica cultivar-group) hemoglobin 1 (hb1), hemoglobin 3 (hb3), and hemoglobin 4 (hb4) genes, complete cds	244	244	44%	8e-61	76%	
AC198891.2	Oryza sativa Japonica Group chromosome 3 clone OJ1175C11, complete sequence	244	244	44%	8e-61	76%	
AC137636.2	Genomic sequence for Oryza sativa, Nipponbare strain, clone OSJNBa0049C20, from chromosome 3, complete sequence	244	244	44%	8e-61	76%	
U76029.1	Oryza sativa hemoglobin 1 (hb1) gene, complete cds	239	239	44%	4e-59	76%	
AY151390.1	Triticum aestivum cultivar Complet hemoglobin Hb1 mRNA, complete cds	884	817	44%	3e-55	98%	
AF231092.1	Zea mays subsp. parviglumis hemoglobin gene, complete cds	185	185	10%	5e-43	94%	
EU966226.1	Zea mays clone 316935 non-symbiotic hemoglobin 2 mRNA, complete cds	180	180	10%	2e-41	93%	
BT390115.1	Zea mays full-length cDNA clone ZM_BFc0066D21 mRNA, complete cds	178	178	10%	8e-41	93%	
DQ244258.1	Zea mays clone 3955 mRNA sequence	178	178	10%	8e-41	93%	
NM_001111496.1	Zea mays hemoglobin (LOC541815), mRNA >gb AF236080.1 AF236080 Zea mays hemoglobin mRNA, complete cds	178	178	10%	8e-41	93%	
AY106330.1	Zea mays PCO112753 mRNA sequence	174	174	10%	1e-39	92%	
AY065016.1	Zea mays hemoglobin gene, complete cds	172	172	10%	4e-39	92%	
EP023496.1	Phyllostachys edulis cDNA clone: bphyem203e02, full insert sequence	182	483	29%	5e-38	98%	
EP101139.1	Phyllostachys edulis cDNA clone: bphyem208d11, full insert sequence	182	483	29%	5e-38	98%	
AC210470.1	Oryza glaberrima clone OG_BB0042O02, complete sequence	139	139	9%	4e-29	88%	
AF335503.1	Oryza sativa (japonica cultivar-group) hemoglobin 2 (hb2) gene, complete cds	139	139	9%	4e-29	88%	
AC197226.2	Oryza sativa Japonica Group chromosome 3 clone OSJNBa0081P02, complete sequence	139	139	9%	4e-29	88%	
U76028.1	Oryza sativa hemoglobin 2 (hb2) gene, complete cds	139	139	9%	4e-29	88%	
CU496284.1	Oryza rufipogon (W1943) cDNA clone: ORW1943S103H20, full insert sequence	132	132	8%	6e-27	90%	
CI833228.1	Oryza sativa (indica cultivar-group) cDNA clone:OSIGCPI026D01, full insert sequence	132	132	8%	6e-27	90%	
CI833927.1	Oryza sativa (indica cultivar-group) cDNA	132	132	8%	6e-27	90%	

	clone:OSIGCPI013P21, full insert sequence						
AK241036.1	Oryza sativa Japonica Group cDNA, clone: J065076O13, full insert sequence	132	132	8%	6e-27	90%	
NM_001055972.1	Oryza sativa Japonica Group Os03g0226200 (Os03g0226200) mRNA, complete cds	132	132	8%	6e-27	90%	
AK121522.1	Oryza sativa Japonica Group cDNA clone:J033028N03, full insert sequence	132	132	8%	6e-27	90%	
U76031.1	Oryza sativa hemoglobin 2 mRNA, complete cds	132	132	8%	6e-27	90%	
NM_021055911.1	Oryza sativa Japonica Group Os03g0233900 (Os03g0233900) mRNA, complete cds	119	119	7%	5e-23	91%	
AK064654.1	Oryza sativa Japonica Group cDNA clone:001-125-F02, full insert sequence	119	119	7%	5e-23	91%	
U78030.1	Oryza sativa hemoglobin 1 mRNA, complete cds	119	119	7%	5e-23	91%	

Alignments

>**gb|U94968.1|HVU94968** Hordeum vulgare hemoglobin gene, complete cds
Length=1173

Score = 2167 bits (1173), Expect = 0.0
Identities = 1173/1173 (100%), Gaps = 0/1173 (0%)
Strand=Plus/Plus

```

Query 1      GAGAACCAAATTAAGCGGGAAGGAAGCCATGTCTGCCGCGAGGGGGCCGTCGTCTTCAG 60
Sbjct 1      GAGAACCAAATTAAGCGGGAAGGAAGCCATGTCTGCCGCGAGGGGGCCGTCGTCTTCAG 60

Query 61     CGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATTCCGCCAA 120
Sbjct 61     CGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATTCCGCCAA 120

Query 121    CCTTGGGCTCCGCTTCTTCTCAAGTACGTACCCTGCCATTTCTTATTCTATGTGGAAGC 180
Sbjct 121    CCTTGGGCTCCGCTTCTTCTCAAGTACGTACCCTGCCATTTCTTATTCTATGTGGAAGC 180

Query 181    AGCGCAATGAAGCCCCCGATGCATCTCCTTGACATGCATGCTGCTGCGTGCGTGCCCTCA 240
Sbjct 181    AGCGCAATGAAGCCCCCGATGCATCTCCTTGACATGCATGCTGCTGCGTGCGTGCCCTCA 240

Query 241    GGATCTTCGAGATCGCGCCGTCGGCGAGGCAGATGTTCCCGTTCCTGCGCGACTCCGACG 300
Sbjct 241    GGATCTTCGAGATCGCGCCGTCGGCGAGGCAGATGTTCCCGTTCCTGCGCGACTCCGACG 300

Query 301    TGCCGCTGGAGACCAACCCCAAGCTCAAGACCCACGCCGTGTCCGTCTTCGTCATGGTAA 360
Sbjct 301    TGCCGCTGGAGACCAACCCCAAGCTCAAGACCCACGCCGTGTCCGTCTTCGTCATGGTAA 360

Query 361    TACACCATGCATCTCCCAACGATCTGCTGCTATGCATTACATATATATGCTTCCATGGCT 420
Sbjct 361    TACACCATGCATCTCCCAACGATCTGCTGCTATGCATTACATATATATGCTTCCATGGCT 420

Query 421    TATCAATGTGTATGGTGTTCGATGAATGGTGCAGACCTGCGAGGCGGCTGCGCAGTTGC 480
Sbjct 421    TATCAATGTGTATGGTGTTCGATGAATGGTGCAGACCTGCGAGGCGGCTGCGCAGTTGC 480

Query 481    GGAAAGCCGGCAAGATCACCGTCAGGGAGACCACCTGAAGAGGCTGGGCGGCACGCACT 540
Sbjct 481    GGAAAGCCGGCAAGATCACCGTCAGGGAGACCACCTGAAGAGGCTGGGCGGCACGCACT 540

Query 541    TGAAATACGGCGTGGCAGATGGCCACTTCGAGGTATGCCCACTTGCCCATTAGCCTTGTG 600
Sbjct 541    TGAAATACGGCGTGGCAGATGGCCACTTCGAGGTATGCCCACTTGCCCATTAGCCTTGTG 600

Query 601    AATTGTACTAGCATGGGGTTCGCTGTTTGATTTTGCAATTGCATTCAAAGTTGTCCTTCAC 660
Sbjct 601    AATTGTACTAGCATGGGGTTCGCTGTTTGATTTTGCAATTGCATTCAAAGTTGTCCTTCAC 660

Query 661    ACGTGTTGCTTCTTCTTCTTCTGCTTGTGTCACAGGTGACGCGGTTTCGCTCTGCTCGAGAC 720
Sbjct 661    ACGTGTTGCTTCTTCTTCTTCTGCTTGTGTCACAGGTGACGCGGTTTCGCTCTGCTCGAGAC 720

Query 721    GATCAAGGAGGCGCTTCCGGCTGACATGTGGGGGCCCGAGATGAGGAACGCGTGGGGCGA 780
Sbjct 721    GATCAAGGAGGCGCTTCCGGCTGACATGTGGGGGCCCGAGATGAGGAACGCGTGGGGCGA 780

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Query 781 GGCATACGATCAACTGGTCGCGGCCATCAAGCAAGAGATGAAGCCAGCTGAGTAGCTCCA 840
          |||
Sbjct 781 GGCATACGATCAACTGGTCGCGGCCATCAAGCAAGAGATGAAGCCAGCTGAGTAGCTCCA 840

Query 841 CCGCACTCATATACCACGCCATTTTCGCCGATTGTCCGTTCAACCTTCCTTGCTTCACCA 900
          |||
Sbjct 841 CCGCACTCATATACCACGCCATTTTCGCCGATTGTCCGTTCAACCTTCCTTGCTTCACCA 900


Query 901 ATTCACCTCATTTACCGTTGTGTTTGTATTGTGTGTTTATGTGCACTAAAGTCTATTGTA 960
          |||
Sbjct 901 ATTCACCTCATTTACCGTTGTGTTTGTATTGTGTGTTTATGTGCACTAAAGTCTATTGTA 960

Query 961 ACACTCAATAAAAGTACAAATTATGCACGATATTCACCCCGCTCTACTTTACAGTCTTTT 1020
          |||
Sbjct 961 ACACTCAATAAAAGTACAAATTATGCACGATATTCACCCCGCTCTACTTTACAGTCTTTT 1020

Query 1021 TTTCTGTTAGAGGAACTCTGATTTAGAGGTTATGCCTCGTACTAGTACATTGCAATACG 1080
          |||
Sbjct 1021 TTTCTGTTAGAGGAACTCTGATTTAGAGGTTATGCCTCGTACTAGTACATTGCAATACG 1080

Query 1081 CTTAGAAAAGATGCTTAAATAAATAAATCAATGTTTTTAGGCACGCGTGCTTATATGTA 1140
          |||
Sbjct 1081 CTTAGAAAAGATGCTTAAATAAATAAATCAATGTTTTTAGGCACGCGTGCTTATATGTA 1140

Query 1141 TCGAGTAAACGTTTAGCCTGTATAAATGAACAC 1173
          |||
Sbjct 1141 TCGAGTAAACGTTTAGCCTGTATAAATGAACAC 1173
```

>gb|U01228.1|U01228  Hordeum vulgare Harrington haemoglobin apoprotein (hb) mRNA,
complete cds
Length=939

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 883 bits (478), Expect = 0.0
Identities = 481/482 (99%), Gaps = 1/482 (0%)
Strand=Plus/Plus

```
Query 693 AGGTGACGCGGTTTCGCTCTGCTCGAGACGATCAAGGAGGCGCTCCGGCTGACATGTGGG 752
          |||
Sbjct 409 AGGTGACGCGGTTTCGCTCTGCTCGAGACGATCAAGGAGGCGCTCCGGCTGACATGTGGG 468

Query 753 GGCCCGAGATGAGGAACGCGTGGGCGAGGCATACGATCAACTGGTCGCGGCCATCAAGC 812
          |||
Sbjct 469 GGCCCGAGATGAGGAACGCGTGGGCGAGGCATACGATCAACTGGTCGCGGCCATCAAGC 528

Query 813 AAGAGATGAAGCCAGCTGAGTAGCTCCACCGCACTCATATACCACGCCATTTTCGCCGAT 872
          |||
Sbjct 529 AAGAGATGAAGCCAGCTGAGTAGCTCCACCGCACTCATATACCACGCCATTTTCGCCGAT 588

Query 873 TGTCCGTTCAACCTTCCTTGCTTCACCAATTCACCTCATTTACCGTTGTGTTTGTATTGT 932
          |||
Sbjct 589 TGTCCGTTCAACCTTCCTTGCTTCACCAATTCACCTCATTTACCGTTGTGTTTGTATTGT 648

Query 933 GTGTTTATGTGCACTAAAGTCTATTGTAACACTCAAT-AAAAGTACAAATTATGCACGAT 991
          |||
Sbjct 649 GTGTTTATGTGCACTAAAGTCTATTGTAACACTCAATCAAAGTACAAATTATGCACGAT 708

Query 992 ATTCACCCCGCTCTACTTTACAGTCTCTGTTAGAGGAACTCTGATTTAGAGGT 1051
          |||
Sbjct 709 ATTCACCCCGCTCTACTTTACAGTTTTTTTTTCTGTTAGAGGAACTCTGATTTAGAGGT 768

Query 1052 TATGCCTCGTACTAGTACATTGCAATACGCTTAGAAAAGATGCTTAAATAAATAAATCAA 1111
          |||
Sbjct 769 TATGCCTCGTACTAGTACATTGCAATACGCTTAGAAAAGATGCTTAAATAAATAAATCAA 828

Query 1112 TGTTTTTTTAGGCACGCGTGCTTATATGTATCGAGTAAACGTTTAGCCTGTATAAATGAAC 1171
          |||
Sbjct 829 TGTTTTTTTAGGCACGCGTGCTTATATGTATCGAGTAAACGTTTAGCCTGTATAAATGAAC 888

Query 1172 AC 1173
          ||
Sbjct 889 AC 890
```

Score = 268 bits (145), Expect = 5e-68
Identities = 145/145 (100%), Gaps = 0/145 (0%)
Strand=Plus/Plus

```
Query 1 GAGAACCAAAATTAAGCGGGAAGGAAGCCATGTCTGCCGCGAGGGGGCCGTCGTCTTCAG 60
          |||
Sbjct 35 GAGAACCAAAATTAAGCGGGAAGGAAGCCATGTCTGCCGCGAGGGGGCCGTCGTCTTCAG 94

Query 61 CGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATTCCGCCAA 120
          |||
Sbjct 95 CGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATTCCGCCAA 154

Query 121 CCTTGGGCTCCGCTTCTTCTCTCAAG 145
          |||
Sbjct 155 CCTTGGGCTCCGCTTCTTCTCTCAAG 179
```

Score = 222 bits (120), Expect = 4e-54
Identities = 120/120 (100%), Gaps = 0/120 (0%)

Score = 213 bits (115), Expect = 2e-51
Identities = 120/122 (99%), Gaps = 1/122 (0%)
Strand=Plus/Plus

Score = 405 bits (219), Expect = 3e-109
Identities = 322/366 (88%), Gaps = 30/366 (8%)
Strand=Plus/Plus

```
Sort alignments for this subject sequence by:
  E value  Score  Percent identity
  Query start position  Subject start position
```

Score = 278 bits (150), Expect = 8e-71
Identities = 241/282 (86%), Gaps = 17/282 (6%)
Strand=Plus/Plus

Score = 226 bits (122), Expect = 3e-55
Identities = 126/128 (99%), Gaps = 0/128 (0%)

Strand=Plus/Plus

```

Query  18  GGAAGGAAGCCATGTCTGCCGCGGAGGGGGCCGTCGTCTTCAGCGAGGAGAAGGAGGCGC  77
      |||
Sbjct  92  GGAAGGAAGCCATGTCTGCCGCGGAGGGAGCCGTCGTGTTTCAGCGAGGAGAAGGAGGCGC  151

Query  78  TGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATTCCGCCAACCTTGGGCTCCGCTTCT  137
      |||
Sbjct  152 TGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATTCCGCCAACCTTGGGCTCCGCTTCT  211

Query  138 TCCTCAAG  145
      |||
Sbjct  212 TCCTCAAG  219

```

Score = 213 bits (115), Expect = 2e-51
 Identities = 120/122 (99%), Gaps = 1/122 (0%)
 Strand=Plus/Plus

```

Query  235 CCTCCAGGATCTTCGAGATCGCGCCGTCGGCGAGGCAGATGTTCCCGTTCCTGCGCGACT  294
      |||
Sbjct  213 CCT-CAAGATCTTCGAGATCGCGCCGTCGGCGAGGCAGATGTTCCCGTTCCTGCGCGACT  271

Query  295 CCGACGTGCCGCTGGAGACCAACCCCAAGCTCAAGACCCACGCCGTGTCCGTCTTCGTCA  354
      |||
Sbjct  272 CCGACGTGCCGCTGGAGACCAACCCCAAGCTCAAGACCCACGCCGTGTCCGTCTTCGTCA  331

Query  355 TG  356
      ||
Sbjct  332 TG  333

```


Score = 195 bits (105), Expect = 8e-46
 Identities = 115/120 (96%), Gaps = 0/120 (0%)
 Strand=Plus/Plus

```

Query  455 GACCTGCGAGGGCGGCTGCGCAGTTGCGGAAAGCCGGCAAGATCACCGTCAGGGAGACCAC  514
      |||
Sbjct  333 GACGTGCGAGGGCTGCTGCGCAGCTGCGGAAAGCCGGGAAGATCACCGTCAGGGAGACCAC  392

Query  515 CCTGAAGAGGCTGGGCGGCACGCACCTTGAAATACGGCGTGGCAGATGGCCACTTCGAGGT  574
      |||
Sbjct  393 CCTGAAGAGGCTGGGCGGCACGCACCTTGAAATACGGCGTGGCAGATGGCCACTTTGAGGT  452

```

>gb|AF335504.1|  Oryza sativa (japonica cultivar-group) hemoglobin 1 (hb1), hemoglobin 3 (hb3), and hemoglobin 4 (hb4) genes, complete cds
 Length=11601

Score = 244 bits (132), Expect = 8e-61
 Identities = 425/557 (77%), Gaps = 57/557 (10%)
 Strand=Plus/Plus

```

Query  55  CTTTCAGCGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATTTC  114
      |||
Sbjct  2410 CTTTCAGCGAGGAGCAGGAGGCGCTGGTGCTCAAGTCATGGGCGATCTTGAAGAAGGATTTC  2469

Query  115 CGCCAACCTTGGGCTCCGCTTCTTCTCAAGTACGTACC--C-TG---C--C-ATTTCT-  164
      |||
Sbjct  2470 CGCCAATATTGCCCTCCGCTTCTTCTTGAAGTATGTACATGCGTGTTACTACCATTCTC  2529

Query  165 TATTCTATGTGGAAGCAGCGCAATGAAGCCCCGATGCATCTCC-TTGA-CA-TGCAT--  219
      |||
Sbjct  2530 T-TT-T-TGCGGAATCAGAG-ATTGG-GTTTGTGAAGCAT-TAAATTGAGCAATGCATTT  2583

Query  220 -GCTG---C-TGCGTG-C-G-T-GCCTCC-AGGATCTTCGAGATCGCGCCGTCGGCGAGG  269
      |||
Sbjct  2584 CGCTGATACATGTGTGTCTGATTGTGTGTAGGATCTTCGAGGTGCGCGCCGTCGGCGAGC  2643

Query  270 CAGATGTTCCCGTTCCTGCGCGACTCCGACGTGCCGCTGGAGACCAACCCCAAGCTCAAG  329
      |||
Sbjct  2644 CAGATGTTCTCGTTCCTGCGCAACTCCGACGTGCCGCTCGAGAAGAACCCCAAGCTCAAG  2703

Query  330 ACCCACGCCGTGTCCGCTCTTCGTATGGTAATAC-ACCATGCATCTCCCAACGATCTGCT  388
      |||
Sbjct  2704 ACCCACGCCATGTCCGCTCTTCGTATGGTAATACTACCAT-CAT-T---ATT--TCAG--  2754


Query  389 GCTA-TGCATTACATATA-TATGCTTC-CA-TGGCTTATCAATGTGTATG-GTGTTCGA  443
      |||
Sbjct  2755 GCAAGTAAATTTGTGTGGTA-G-TAGACACTGAC--AG-AATGTGTGCGTGCCTCGCGA  2809

Query  444 TGAATGG-T---GCAGACCTGCGAGGCGGCTGCGCAGTTGCGGAAAGCCGGCAAGATCAC  499
      |||
Sbjct  2810 TCAATCGATATTGCAGACATGCGAGGCCGCCGCGCAGCTGCGGAAAGCCGGGAAGGTCAC  2869

Query  500 CGTCAGGGAGACCAACCTGAAGAGGCTGGGCGGCACGCACCTTGAAATACGGCGT-GGCAG  558
      |||
Sbjct  2870 CGTGAGAGACACCAACCTCAAGAGGCTCGGCGCCACGCACCTCAAGTACGGCGTCCG-AG  2928

Query  559 ATGGCCACTTCGAGGTA  575
      |||
Sbjct  2929 ACGCCACTTCGAGGTA  2945

```

>gb|AC103891.2|  Oryza sativa Japonica Group chromosome 3 clone OJ1175C11, complete sequence
 Length=123620

Score = 244 bits (132), Expect = 8e-61
 Identities = 425/557 (77%), Gaps = 57/557 (10%)
 Strand=Plus/Minus

```

Query 55      CTTACAGCGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATTC 114
              |||
Sbjct 19766   CTTACAGCGAGGAGCAGGAGGCGCTGGTGCTCAAGTCATGGGCGATCTTGAAGAAGGATTC 19707

Query 115     CGCCAACCTTGGGCTCCGCTTCTTCTCAAGTACGTACC--C-TG---C--C-ATTTCT- 164
              |||
Sbjct 19706   CGCCAATATTGCCCTCCGCTTCTTCTTGAAGTATGTACATGCGTGTACTACCATTCTC 19647

Query 165     TATTCTATGTGGAAGCAGCGCAATGAAGCCCCGATGCATCTCC-TTGA-CA-TGCAT-- 219
              |||
Sbjct 19646   T-TT-T-TGCGGAATCAGAG-ATTGG-GTTTGTGAAGCAT-TAAATTGAGCAATGCATTT 19593

Query 220     -GCTG---C-TGCGTG-C-G-T-GCCTCC-AGGATCTTCGAGATCGCGCCGTCGGCGAGG 269
              |||
Sbjct 19592   CGCTGATACATGTGTCTGATTGTGTTGTAGGATCTTCGAGGTCGCGCCGTCGGCGAGC 19533

Query 270     CAGATGTTCCCGTTTCTGCGCACTCCGACGTGCCGCTGGAGACCAACCCCAAGCTCAAG 329
              |||
Sbjct 19532   CAGATGTTCTCGTTCTTCTGCGCACTCCGACGTGCCGCTCGAGAAGAACCCCAAGCTCAAG 19473

Query 330     ACCCACGCCGTGTCCGTCTTCGTTCATGGTAATAC-ACCATGCATCTCCCAACGATCTGCT 388
              |||
Sbjct 19472   ACCCACGCCATGTCCGTCTTCGTTCATGGTAATACTACCAT-CAT-T---ATT--TCAG-- 19422

Query 389     GCTA-TGCATTACATATA-TATGCTTC-CA-TGGCTTATCAATGTGTATG-GTGTTCGCA 443
              |||
Sbjct 19421   GCAAGTAAATTGTTGTGGTA-G-TAGACACTGAC--AG-AATGTGTGCGTGCCTCGCGA 19367

Query 444     TGAATGG-T---GCAGACCTGCGAGGCGGCTGCGCAGTTGCGGAAAGCCGGCAAGATCAC 499
              |||
Sbjct 19366   TCAATCGATATTGCAGACATGCGAGGCCGCCGCGCAGCTGCGGAAAGCCGGGAAGGTCAC 19307

Query 500     CGTCAGGGAGACCACCTGAAGAGGCTGGGCGGCACGCACTTGAAATACGGCGT-GGCAG 558
              |||
Sbjct 19306   CGTGAGAGACACCACCTCAAGAGGCTCGGCGCCACGCACCTCAAGTACGGCGTCGG-AG 19248

Query 559     ATGGCCACTTTCGAGGTA 575
              |||
Sbjct 19247   ACGCCCACTTCGAGGTA 19231
  
```

>gb|AC137696.2|  Genomic sequence for *Oryza sativa*, Nipponbare strain, clone OSJNBa0049C20, from chromosome 3, complete sequence
 Length=136098

Score = 244 bits (132), Expect = 8e-61
 Identities = 425/557 (77%), Gaps = 57/557 (10%)
 Strand=Plus/Minus

```

Query 55      CTTACAGCGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATTC 114
              |||
Sbjct 131739   CTTACAGCGAGGAGCAGGAGGCGCTGGTGCTCAAGTCATGGGCGATCTTGAAGAAGGATTC 131680

Query 115     CGCCAACCTTGGGCTCCGCTTCTTCTCAAGTACGTACC--C-TG---C--C-ATTTCT- 164
              |||
Sbjct 131679   CGCCAATATTGCCCTCCGCTTCTTCTTGAAGTATGTACATGCGTGTACTACCATTCTC 131620

Query 165     TATTCTATGTGGAAGCAGCGCAATGAAGCCCCGATGCATCTCC-TTGA-CA-TGCAT-- 219
              |||
Sbjct 131619   T-TT-T-TGCGGAATCAGAG-ATTGG-GTTTGTGAAGCAT-TAAATTGAGCAATGCATTT 131566

Query 220     -GCTG---C-TGCGTG-C-G-T-GCCTCC-AGGATCTTCGAGATCGCGCCGTCGGCGAGG 269
              |||
Sbjct 131565   CGCTGATACATGTGTCTGATTGTGTTGTAGGATCTTCGAGGTCGCGCCGTCGGCGAGC 131506

Query 270     CAGATGTTCCCGTTTCTGCGCACTCCGACGTGCCGCTGGAGACCAACCCCAAGCTCAAG 329
              |||
Sbjct 131505   CAGATGTTCTCGTTCTTCTGCGCACTCCGACGTGCCGCTCGAGAAGAACCCCAAGCTCAAG 131446

Query 330     ACCCACGCCGTGTCCGTCTTCGTTCATGGTAATAC-ACCATGCATCTCCCAACGATCTGCT 388
              |||
Sbjct 131445   ACCCACGCCATGTCCGTCTTCGTTCATGGTAATACTACCAT-CAT-T---ATT--TCAG-- 131395

Query 389     GCTA-TGCATTACATATA-TATGCTTC-CA-TGGCTTATCAATGTGTATG-GTGTTCGCA 443
              |||
Sbjct 131394   GCAAGTAAATTGTTGTGGTA-G-TAGACACTGAC--AG-AATGTGTGCGTGCCTCGCGA 131340

Query 444     TGAATGG-T---GCAGACCTGCGAGGCGGCTGCGCAGTTGCGGAAAGCCGGCAAGATCAC 499
              |||
Sbjct 131339   TCAATCGATATTGCAGACATGCGAGGCCGCCGCGCAGCTGCGGAAAGCCGGGAAGGTCAC 131280

Query 500     CGTCAGGGAGACCACCTGAAGAGGCTGGGCGGCACGCACTTGAAATACGGCGT-GGCAG 558
              |||
Sbjct 131279   CGTGAGAGACACCACCTCAAGAGGCTCGGCGCCACGCACCTCAAGTACGGCGTCGG-AG 131221

Query 559     ATGGCCACTTTCGAGGTA 575
              |||
Sbjct 131220   ACGCCCACTTCGAGGTA 131204
  
```

>gb|U76029.1|OSU76029 *Oryza sativa* hemoglobin 1 (hb1) gene, complete cds
 Length=827

Score = 239 bits (129), Expect = 4e-59
 Identities = 424/557 (77%), Gaps = 57/557 (10%)
 Strand=Plus/Plus

```

Query 55  CTTACGCGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATT 114
          |||
Sbjct 39  CTTACGCGAGGAGCAGGAGGCGCTGGTGCTCAAGTCATGGGCGATCTTGAAGAAGGATT 98

Query 115 CGCCAACCTTGGGCTCCGCTTCTTCCTCAAGTACGTACC--C-TG---C--C-ATTTCT- 164
          |||
Sbjct 99  CGCCAATATTGCCCTCCGCTTCTTCTTGAAGTATGTACATGCGTGTACTACCATTTCTC 158

Query 165 TATTCTATGTGGAAGCAGCGCAATGAAGCCCCGATGCATCTCC-TTGA-CA-TGCAT-- 219
          |||
Sbjct 159 T-TT-T-TGCCGAATCAGAG-ATTGG-GTTTGTGAAGCAT-TAAATTGAGCAATGCATTT 212

Query 220 -GCTG---C-TGCGTG-C-G-T-GCCTCC-AGGATCTTCGAGATCGCGCCGTCGGCGAGG 269
          |||
Sbjct 213 CGCTGATACATGTGTGTCTGATTGTGTGTGTAGGATCTTCGAGGTCGCGCCGTCGGCGAGC 272

Query 270 CAGATGTTCCCGTTCCTGCGCGACTCCGACGTGCCGCTGGAGACCAACCCCAAGCTCAAG 329
          |||
Sbjct 273 CAGATGTTCTCGTTCCTGCGAAACTCCGACGTGCCGCTCGAGAAGAACCCCAAGCTCAAG 332


Query 330 ACCCAGCGCGTGTCCGCTCTTCGTCATGGTAATAC-ACCATGCATCTCCCAACGATCTGCT 388
          |||
Sbjct 333 ACCCAGGCCATGTCCGCTCTTCGTCATGGTAATACTACCAT-CAT-T---ATT--TCAG-- 383

Query 389 GCTA-TGCATTACATATA-TATGCTTC-CA-TGGCTTATCAATGTGTATG-GTGTTCGA 443
          |||
Sbjct 384 GCAAGTAAATTTGTGTGGTA-G-TAGACACTGAC--AG-AATGTGTGCGTGCCTCGCGA 438

Query 444 TGAATGG-T---GCAGACCTGCGAGGCGGCTGCGCAGTTGCGGAAAGCCGGCAAGATCAC 499
          |||
Sbjct 439 TCAATCGATATTGCAGACATGCGAGGCCGCGCGCAGCTGCGGAAAGCCGGGAAGGTCAC 498

Query 500 CGTCAGGGAGACCACCCTGAAGAGGCTGGGCGGCACGCACCTTGAAATACGGCGT-GGCAG 558
          |||
Sbjct 499 CGTGAGAGACACCACCCTCAAGAGGCTCGGCGCCACGCACCTCAAGTACGGCGTCGG-AG 557

Query 559 ATGGCCACTTCGAGGTA 575
          |||
Sbjct 558 ACGCCCACTTCGAGGTA 574
  
```

>gb|AY151390.1|  Triticum aestivum cultivar Complet hemoglobin Hb1 mRNA, complete
 cds
 Length=516

GENE ID: 543085 LOC543085 | hemoglobin Hb1 [Triticum aestivum]
 (10 or fewer PubMed links)

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 226 bits (122), Expect = 3e-55
 Identities = 138/146 (95%), Gaps = 0/146 (0%)
 Strand=Plus/Plus

```

Query 693 AGGTGACGCGGTTTCGCTCTGCTCGAGACGATCAAGGAGGCGCTTCCGGCTGACATGTGGG 752
          |||
Sbjct 362 AGGTGACGCGGTTTCGCTCTGCTCGAGACGATCAAGGAGGCGCTTCCGGCGGACATGTGGG 421

Query 753 GGCCCGAGATGAGGAACGCGTGGGGCGAGGCATACGATCAACTGGTTCGCGGCCATCAAGC 812
          |||
Sbjct 422 GGCCCGAGATGAGGAACGCGTGGGGCGAAGCCTACGACCAACTGGTTCGCGGCCATCAAGC 481

Query 813 AAGAGATGAAGCCAGCTGAGTAGCTC 838
          |||
Sbjct 482 AAGAGATGAAGCCCTCTGAATAGCTC 507
  
```

Score = 213 bits (115), Expect = 2e-51
 Identities = 120/122 (99%), Gaps = 1/122 (0%)
 Strand=Plus/Plus

```

Query 235 CCTCCAGGATCTTCGAGATCGCGCCGTCGGCGAGGCAGATGTTCCCGTTCCTGCGCGACT 294
          |||
Sbjct 126 CCT-CAAGATCTTCGAGATCGCGCCGTCGGCGAGGCAGATGTTCCCGTTCCTGCGCGACT 184

Query 295 CCGACGTGCGCTGGAGACCAACCCCAAGCTCAAGACCCACGCCGTGTCCTGCTTCGTCA 354
          |||
Sbjct 185 CCGACGTGCGCTGGAGACCAACCCCAAGCTCAAGACCCACGCCGTGTCCTGCTTCGTCA 244

Query 355 TG 356
          ||
Sbjct 245 TG 246
  
```

Score = 209 bits (113), Expect = 3e-50
 Identities = 124/129 (97%), Gaps = 1/129 (0%)
 Strand=Plus/Plus

```



Query 17  GGGAAAGGAAGCCATGTCTGCCGCGGAGGGGGCCGTCGTCTTCAGCGAGGAGAAGGAGCG 76
          |||
Sbjct 5  GGG-AGGAAGCCATGTCTGCCGCGGAGAGGCCGTCGTGTTACGCGAGGAGAAGGATGCG 63
  
```



```

Sbjct 301      ||| ||| ||||||||||||||||||||||||||||||||||||||| 359
          CTCAAGG-TCTTCGAGATCGCGCCGTCGGCGAAGCAGATGTTCTCGTTCCTGCGCGACTC
Query 296      CGACGTGCCGCTGGAGACCAACCCCAAGCTCAAGACCCACGCCGTGTCCTGTCAT 355
          |||||||||||||||||||||||||||||||||||||||
Sbjct 360      CGACGTGCCGCTGGAGAAGAACCCCAAGCTCAAGACGCACGCCATGTCCGTCTTCGTCAT 419
          |||||||||||||||||||||||||||||||||||||||
Query 356      G 356
          |
Sbjct 420      G 420

```

>ref|NM_00111496.1|  Zea mays hemoglobin (LOC541815), mRNA
 gb|AF236080.1|AF236080  Zea mays hemoglobin mRNA, complete cds
 Length=885

GENE ID: 541815 LOC541815 | hemoglobin [Zea mays] (10 or fewer PubMed links)

Score = 178 bits (96), Expect = 8e-41
 Identities = 113/121 (94%), Gaps = 1/121 (0%)
 Strand=Plus/Plus

```

Query 236      CTCCAGGATCTTCGAGATCGCGCCGTCGGCGAGGCAGATGTTCCCGTTCCTGCGCGACTC 295
          ||| ||| |||||||||||||||||||||||||||||||||||
Sbjct 292      CTCAAGG-TCTTCGAGATCGCGCCGTCGGCGAAGCAGATGTTCTCGTTCCTGCGCGACTC 350
          ||| ||| |||||||||||||||||||||||||||||||||||
Query 296      CGACGTGCCGCTGGAGACCAACCCCAAGCTCAAGACCCACGCCGTGTCCTGTCAT 355
          |||||||||||||||||||||||||||||||||||||||
Sbjct 351      CGACGTGCCGCTGGAGAAGAACCCCAAGCTCAAGACGCACGCCATGTCCGTCTTCGTCAT 410
          |||||||||||||||||||||||||||||||||||||||
Query 356      G 356
          |
Sbjct 411      G 411

```

>gb|AY108330.1|  Zea mays PC0112753 mRNA sequence
 Length=1007

Score = 174 bits (94), Expect = 1e-39
 Identities = 113/122 (93%), Gaps = 1/122 (0%)
 Strand=Plus/Plus

```

Query 235      CCTCCAGGATCTTCGAGATCGCGCCGTCGGCGAGGCAGATGTTCCCGTTCCTGCGCGACT 294
          ||| ||| |||||||||||||||||||||||||||||||||||
Sbjct 283      CCTCAAGG-TCTTCGAGATCGCGCCGTCGGCGAAGCAGATGTTCTCGTTCCTGCGCGACT 341
          ||| ||| |||||||||||||||||||||||||||||||||||
Query 295      CCGACGTGCCGCTGGAGACCAACCCCAAGCTCAAGACCCACGCCGTGTCCTGTCATCA 354
          |||||||||||||||||||||||||||||||||||||||
Sbjct 342      CCGACGTGCCGCTAGAGAAGAACCCCAAGCTCAAGACGCACGCCATGTCCGTCTTCGTCAT 401
          |||||||||||||||||||||||||||||||||||||||
Query 355      TG 356
          ||
Sbjct 402      TG 403

```

>gb|AY005818.1| Zea mays hemoglobin gene, complete cds
 Length=874

Score = 172 bits (93), Expect = 4e-39
 Identities = 113/122 (93%), Gaps = 3/122 (2%)
 Strand=Plus/Plus

```

Query 239      CAGGATCTTCGAGATCGCGCCGTCGGC-GAGGCAGATGTTCCCGTTCCTGCGCGACTCCG 297
          ||| ||| |||||||||||||||||||||||||||||||||||
Sbjct 255      CAGG-TCTTCGAGATCGCGCCGTCGGCGGA-GCAGATGTTCTCGTTCCTGCGCGACTCCG 312
          ||| ||| |||||||||||||||||||||||||||||||||||
Query 298      ACGTGCCGCTGGAGACCAACCCCAAGCTCAAGACCCACGCCGTGTCCTGTCATGG 357
          |||||||||||||||||||||||||||||||||||||||
Sbjct 313      ACGTGCCGCTAGAGAAGAACCCCAAGCTCAAGACGCACGCCATGTCCGTCTTCGTCATGG 372
          |||||||||||||||||||||||||||||||||||||||
Query 358      TA 359
          ||
Sbjct 373      TA 374

```

>emb|FP098496.1| Phyllostachys edulis cDNA clone: bphyem203e02, full insert sequence
 Length=2533

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 169 bits (91), Expect = 5e-38
 Identities = 127/144 (89%), Gaps = 4/144 (2%)
 Strand=Plus/Plus

```

Query 693      AGGTGACGCGGTTTCGCTCTGCTCGAGACGATCAAGGAGGC-GCTTCCGGCTGACATGTGG 751
          ||| ||| |||||||||||||||||||||||||||||||||||
Sbjct 2043      AGGTGACAAGGTTTCGCGCTGCTTGAGACGATAAAGGAGGCTG-TTCCGGCTGACATGT-G 2100
          ||| ||| |||||||||||||||||||||||||||||||||||
Query 752      GGGCCC-GAGATGAGGAACGCTGGGGCGAGGCATACGATCAACTGGTCGCGGCCATCAA 810
          ||| ||| |||||||||||||||||||||||||||||||||||
Sbjct 2101      GGGCCCCGAGATGAAGAACGCTTGGGGCGAAGCCTACGACCACCTGGTCGCGGCCATCAA 2160
          ||| ||| |||||||||||||||||||||||||||||||||||
Query 811      GCAAGAGATGAAGCCAGCTGAGTA 834
          ||| ||| |||||||||||||||||| ||| |||

```


Query	97	CATCATGAAGAAGGATTCCGCCAACCTTGGGCTCCGCTTCTTCTCTCAAGTACGTAC	152
Subject	20253	CATCATGAAGAAGGATTCCGCCAACATTGGACTCCGCTTCTTCTTGAAGTATGTAC	20198

```
>gb|AF335503.1|  Oryza sativa (japonica cultivar-group) hemoglobin 2 (hb2) gene, complete cds  
Length=3793
```

GENE ID: 4332123 Os03g0226200 | Os03g0226200 [Oryza sativa Japonica Group]
(10 or fewer PubMed links)

Score = 139 bits (75), Expect = 4e-29
Identities = 103/116 (89%), Gaps = 4/116 (3%)
Strand=Plus/Plus

```

Query    39      CGGAGGGG-GCCGTC-GTCTTCAGCGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGC   96
Sbjct    992      CGG-GGGGAGCGGTGAG-CTTCAGCGAGGAGCAGGAGGCGCTTGTGCTCAAGTCGTGGGC   1049

Query    97      CATCATGAAGAAGGATTCCGCCAACCTTGGGCTCCGCTTCTTCTCAAGTACGTAC   152
Sbjct    1050     CATCATGAAGAAGGATTCCGCCAACATTGGACTCCGCTTCTTCTGAAGTATGTAC   1105

```

```
>gb|AC107226.2| Oryza sativa Japonica Group chromosome 3 clone OSJNBa0081P02,
complete sequence
Length=162425
```

Score = 139 bits (75), Expect = 4e-29
Identities = 103/116 (89%), Gaps = 4/116 (3%)
Strand=Plus/Minus

Query	39	CGGAGGGG-GCCGTC-GTCTTCAGCGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGC	96
Sbjct	137007	CGG-GGGGAGCGGTACAG-CTTCAGCGAGGAGCAGGAGGCGCTTGTGCTCAAGTCGTGGGC	136950
Query	97	CATCATGAAGAAGGATTCCGCCAACCTTTGGGCTCCGCTTCTTCTCAAGTACGTAC	152
Sbjct	136949	CATCATGAAGAAGGATTCCGCCAACATTGGACTCCGCTTCTTCTGAAGTATGTAC	136894

```
>gb|U76028.1|OSU76028 Oryza sativa hemoglobin 2 (hb2) gene, complete cds
Length=836
```

Score = 139 bits (75), Expect = 4e-29
Identities = 103/116 (89%), Gaps = 4/116 (3%)
Strand=Plus/Plus

```

Query    39      CGGAGGGG-GCCGTC-GTCTTCAGCGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGC   96
Sbjct    32      CGG-GGGGAGCGGTACG-CTTCAGCGAGGAGCAGAGAGGCGCTTGCTCAAGTCGTGGGC   89

Query    97      CATCATGAAGAAGGATTCCGCCAACCTTGGGCTCCGCTTCTTCCTCAAGTACGTAC   152
Sbjct    90      CATCATGAAGAAGGATTCCGCCAACATTGGAAGTCCGCTTCTTCTGAAGTATGTAC   145

```

>emb|CU406294.1| Oryza rufipogon (W1943) cDNA clone: ORW1943S103H20, full insert
sequence
Length=687


Score = 132 bits (71), Expect = 6e-27
Identities = 93/103 (91%), Gaps = 4/103 (3%)
Strand=Plus/Plus

```

Query    39      CGGAGGGG-GCCGTC-GTCTTCAGCGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGC   96
Sbjct    112     CGG-GGGGAGCGGTCAG-CTTCAGCGAGGAGCAGGAGGCGCTTGTGCTCAAGTCGTGGGC   169

Query    97      CATCATGAAGAAGGATTCCGCCAACCTTGGGCTCCGCTTCTTC   139
Sbjct    170     CATCATGAAGAAGGATTCCGCCAACATTGGACTCCGCTTCTTC   212

```

```
>emb|CT833928.1|  Oryza sativa (indica cultivar-group) cDNA clone:OSIGCPI026D01,
full insert sequence
Length=762
```


Score = 132 bits (71), Expect = 6e-27
Identities = 93/103 (91%), Gaps = 4/103 (3%)
Strand=Plus/Plus

```

Query    39      CGGAGGGG-GCCGTC-GTCTTCAGCGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGC   96
Sbjct   107      CGG-GGGGAGCGGTCAG-CTTCAGCGAGGAGCAGGAGGCGCTTGTGCTCAAGTCGTGGGC   164

Query    97      CATCATGAAGAAGGATTCCGCCAACCTTGGGCTCCGCTTCTTC   139
Sbjct   165      CATCATGAAGAAGGATTCCGCCAACATTGGACTCCGCTTCTTC   207

```


```
>emb|CT833927.1|  Oryza sativa (indica cultivar-group) cDNA clone:OSIGCPI013P21,
full insert sequence
Length=770
```


Strand=Plus/Plus

```

Query  55  CTTCAGCGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATTC  114
          |||
Sbjct  139  CTTCAGCGAGGAGCAGGAGGCGCTGGTGCTCAAGTCATGGGCGATCTTGAAGAAGGATTC  198
          |||
Query  115  CGCCAACCTTGGGCTCCGCTTCTTC  139
          |||
Sbjct  199  CGCCAATATTGCCCTCCGCTTCTTC  223
          |||

```

>**dbj|AK064054.1|**  *Oryza sativa Japonica Group* cDNA clone:001-125-F02, full insert
sequence
Length=799


GENE ID: 4332166 Os03g0233900 | Os03g0233900 [*Oryza sativa Japonica Group*]
(10 or fewer PubMed links)

Score = 119 bits (64), Expect = 5e-23
Identities = 78/85 (92%), Gaps = 0/85 (0%)
Strand=Plus/Plus

```

Query  55  CTTCAGCGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATTC  114
          |||
Sbjct  139  CTTCAGCGAGGAGCAGGAGGCGCTGGTGCTCAAGTCATGGGCGATCTTGAAGAAGGATTC  198
          |||
Query  115  CGCCAACCTTGGGCTCCGCTTCTTC  139
          |||
Sbjct  199  CGCCAATATTGCCCTCCGCTTCTTC  223
          |||

```

>**gb|U76030.1|OSU76030**  *Oryza sativa* hemoglobin 1 mRNA, complete cds
Length=812

Score = 119 bits (64), Expect = 5e-23
Identities = 78/85 (92%), Gaps = 0/85 (0%)
Strand=Plus/Plus

```

Query  55  CTTCAGCGAGGAGAAGGAGGCGCTGGTGCTCAAGTCATGGGCCATCATGAAGAAGGATTC  114
          |||
Sbjct  136  CTTCAGCGAGGAGCAGGAGGCGCTGGTGCTCAAGTCATGGGCGATCTTGAAGAAGGATTC  195
          |||
Query  115  CGCCAACCTTGGGCTCCGCTTCTTC  139
          |||
Sbjct  196  CGCCAATATTGCCCTCCGCTTCTTC  220
          |||

```